

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Hillman, Jennifer L.  
Corley, Neil C.  
Baughn, Mariah R.

(ii) TITLE OF INVENTION: DELTA 1-PYRROLINE-5-CARBOXYLATE REDUCTASE  
HOMOLOG

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: Windows  
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED  
(B) FILING DATE: HEREWITH  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cerrone, Michael C  
(B) REGISTRATION NUMBER: 39,132  
(C) REFERENCE/DOCKET NUMBER: PF-0532 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555  
(B) TELEFAX: 650-855-0572  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSNON01

(B) CLONE: 2278458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ser	Val	Gly	Phe	Ile	Gly	Ala	Gly	Gln	Leu	Ala	Tyr	Arg	Phe	Thr
1				5					10					15	
Ala	Ala	Gly	Ile	Leu	Ser	Ala	His	Lys	Ile	Ile	Ala	Ser	Ser	Pro	Glu
			20					25					30		
Met	Asn	Leu	Pro	Thr	Val	Ser	Ala	Leu	Arg	Lys	Met	Gly	Val	Asn	Leu
	35						40					45			
Thr	Arg	Ser	Asn	Lys	Glu	Thr	Val	Lys	His	Ser	Asp	Val	Leu	Phe	Leu
	50					55					60				
Ala	Val	Lys	Pro	His	Ile	Ile	Pro	Phe	Ile	Leu	Asp	Glu	Ile	Gly	Ala
65					70					75					80
Asp	Val	Gln	Ala	Arg	His	Ile	Val	Val	Ser	Cys	Ala	Ala	Gly	Val	Thr
				85					90					95	
Ile	Ser	Ser	Val	Glu	Lys	Lys	Leu	Met	Ala	Phe	Gln	Pro	Ala	Pro	Lys
			100					105					110		
Val	Ile	Arg	Cys	Met	Thr	Asn	Thr	Pro	Val	Val	Val	Gln	Glu	Gly	Ala
	115						120					125			
Thr	Val	Tyr	Ala	Thr	Gly	Thr	His	Ala	Leu	Val	Glu	Asp	Gly	Gln	Leu
	130						135					140			
Leu	Glu	Gln	Leu	Met	Ser	Ser	Val	Gly	Phe	Cys	Thr	Glu	Val	Glu	Glu
145					150					155					160
Asp	Leu	Ile	Asp	Ala	Val	Thr	Gly	Leu	Ser	Gly	Ser	Gly	Pro	Ala	Tyr
			165						170					175	
Ala	Phe	Met	Ala	Leu	Asp	Ala	Asp	Gly	Gly	Val	Lys	Met	Gly	Leu	Pro
			180					185					190		
Arg	Arg	Leu	Ala	Ile	Gln	Leu	Gly	Ala	Gln	Ala	Leu	Leu	Gly	Ala	Ala
	195						200						205		
Lys	Met	Leu	Leu	Asp	Ser	Glu	Gln	His	Pro	Cys	Gln	Leu	Lys	Asp	Asn
	210					215					220				
Val	Cys	Ser	Pro	Gly	Gly	Ala	Thr	Ile	His	Ala	Leu	His	Phe	Leu	Glu
225					230					235					240
Ser	Gly	Gly	Phe	Arg	Ser	Leu	Leu	Ile	Asn	Ala	Val	Glu	Ala	Ser	Cys
			245						250					255	
Ile	Arg	Thr	Arg	Glu	Leu	Gln	Ser	Met	Ala	Asp	Gln	Glu	Lys	Ile	Ser
			260					265					270		
Pro	Ala	Ala	Leu	Lys	Lys	Thr	Leu	Leu	Asp	Arg	Val	Lys	Leu	Glu	Ser
	275						280					285			
Pro	Thr	Val	Ser	Thr	Leu	Thr	Pro	Ser	Ser	Pro	Gly	Lys	Leu	Leu	Thr
	290					295					300				
Arg	Ser	Leu	Ala	Leu	Gly	Gly	Lys	Lys	Asp						
305					310										

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNON01
- (B) CLONE: 2278458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCGCCATCAG	CCGCCCCGGA	GATATCCGCC	GGGGGAGAAT	AGGGTTGCAC	CATCCCAGAA	60
GCTGCTGTTA	GCTCGCCGGT	CCTCGGCACG	CCGCCCCGTT	CCCCCTGCGC	TGTCCGCCCT	120

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TCCCCTAGCG TTACTTCCGG TCCCTCGCTG AGGGGGTTTCG TGCGGCTCCC AGGAGGCGTG 180
AACCGCGGAC CATGAGCGTG GGCTTCATCG GGGCCGGCCA GCTGGCCTAT GCTCTGGCGC 240
GGGGCTTCAC GGCCGCAGGC ATCCTGTCTG CTCACAAGAT AATAGCCAGC TCCCCAGAAA 300
TGAACCTGCC CACGGTGTCC GCGCTCAGGA AGATGGGTGT GAACCTGACA CGCAGCAACA 360
AGGAGACGGT GAAGCACAGC GACGTCCTGT TTCTGGCTGT GAAGCCACAT ATCATCCCCT 420
TCATCCTGGA TGAGATTGGG GCCGACGTGC AAGCCAGACA CATCGTGGTC TCCTGTGCGG 480
CTGGTGTAC CATCAGCTCT GTGGAGAAGA AGCTGATGGC ATTCCAGCCA GCCCCCAAAG 540
TGATTGCTG CATGACCAAC ACACCTGTGG TAGTGCAGGA AGGCGCTACA GTGTACGCCA 600
CGGGCACCCA TGCCCTGGTG GAGGATGGGC AGCTCCTGGA GCAGCTCATG AGCAGCGTGG 660
GCTTCTGCAC TGAGGTGGAA GAGGACCTCA TCGATGCCGT CACGGGGCTC AGTGGCAGCG 720
GGCCTGCCTA TGCATTTCATG GCTCTGGACG CATTGGCTGA TGGTGGGGTG AAGATGGGTT 780
TGCCACGGCG CCTGGCAATC CAACTCGGGG CCCAGGCTTT GCTGGGAGCT GCCAAGATGC 840
TGCTGGACTC GGAGCAGCAT CCATGCCAGC TTAAGGACAA TGTCTGCTCC CCTGGGGGAG 900
CCACCATCCA CGCCCTGCAC TTTCTAGAGA GTGGGGGCTT CCGCTCTCTG CTCATCAATG 960
CAGTTGAGGC CTCCTGTATC CGAACACGAG AGCTACAGTC CATGGCCGAC CAAGAAAAGA 1020
TCTCCCCAGC TGCCCTTAAG AAGACCCCTCT TAGACAGAGT GAAGCTGGAA TCCCCCACAG 1080
TCTCCACACT GACCCCTCC AGCCCAGGGA AGCTCCTCAC AAGAAGCCTG GCCCTGGGAG 1140
GCAAGAAGGA CTAAGGCAGC ATCTGTCCCC TCTGTGATTC AGAGCCCTTA GTTGAGAGCC 1200
CCTGCCGCCC CTGCCACCCC CCTGCCCCGC TCCACCATTT GCCCTCCTC AGCTGTGCAA 1260
GGAGAAAGCA TGCTTAGGAA GTTTTCAGGT CTTGTGATA AAACCTCCTT AAATCTGTTC 1320
AGACCAAGCA ATGCGAGCTT CCTCTCCTGT CCCATGTTGG AAGTTGCTCT GAAGGGGTGG 1380
TAGATGCTGG AAGCCAGACA CAACCCTGCG TACGCTGCTC AGTTGGTGGA GACTGGGGCT 1440
GGGACTGGAG TCAGCCCAGC TGGGAGGAGG GGCTGGGGAG GATCTGCAGC TGAAGCCCGA 1500
GGCAGGGTTG GTGTGATGCC AAGGCAAAGT GGTGAGGAGA AAACAGGAAA CGGGCTTTCT 1560
CTGAATTGGT AAATGGGAAA GAAGTGAGCA ACTTAAGATT GTCACAAATTA ATCAACAAGT 1620
TACAGGATTA GACTGGGTTT ATATTTAACT CTTGCTTCAT AGGTGTACCA TTTAAAGAGT 1680
GTTATTTAAT GCTAAGTTTA ACTGCTTTAA TAAAGTTTAT TTTTAAATAT CAAAAAATAA 1740
AA

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GENBANK
- (B) CLONE: 189498

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Ser Val Gly Phe Ile Gly Ala Gly Gln Leu Ala Phe Ala Lys Gly
 1           5           10           15
Phe Thr Ala Ala Gly Val Leu Ala Ala His Lys Ile Met Ala Ser Ser
          20          25          30
Pro Asp Met Asp Leu Ala Thr Val Ser Ala Leu Arg Lys Met Gly Val
          35          40          45
Lys Leu Thr Pro His Asn Lys Glu Thr Val Gln His Ser Asp Val Leu
          50          55          60
Phe Leu Ala Val Lys Pro His Ile Ile Pro Phe Ile Leu Asp Glu Ile
65          70          75          80
Gly Ala Asp Ile Glu Asp Arg His Ile Val Val Ser Cys Ala Ala Gly
          85          90          95
Val Thr Ile Ser Ser Ile Glu Lys Lys Leu Ser Ala Phe Arg Pro Ala
          100         105         110
Pro Arg Val Ile Arg Cys Met Thr Asn Thr Pro Val Val Val Arg Glu
          115         120         125
Gly Ala Thr Val Tyr Ala Thr Gly Thr His Ala Gln Val Glu Asp Gly
          130         135         140

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Arg	Leu	Met	Glu	Gln	Leu	Leu	Ser	Thr	Val	Gly	Phe	Cys	Thr	Glu	Val
145					150					155					160
Glu	Glu	Asp	Leu	Ile	Asp	Ala	Val	Thr	Gly	Leu	Ser	Gly	Ser	Gly	Pro
				165					170						175
Ala	Tyr	Ala	Phe	Thr	Ala	Leu	Asp	Ala	Asp	Gly	Gly	Val	Lys	Met	Gly
			180					185					190		
Leu	Pro	Arg	Arg	Leu	Ala	Val	Arg	Leu	Gly	Ala	Gln	Ala	Leu	Leu	Gly
		195					200					205			
Ala	Ala	Lys	Met	Leu	Leu	His	Ser	Glu	Gln	His	Pro	Gly	Gln	Leu	Lys
		210				215					220				
Asp	Asn	Val	Ser	Ser	Pro	Gly	Gly	Ala	Thr	Ile	His	Ala	Leu	His	Val
225					230					235					240
Leu	Glu	Ser	Gly	Gly	Phe	Arg	Ser	Leu	Leu	Ile	Asn	Ala	Val	Glu	Ala
				245					250					255	
Ser	Cys	Ile	Arg	Thr	Arg	Glu	Leu	Gln	Ser	Met	Ala	Asp	Gln	Glu	Gln
			260					265					270		
Val	Ser	Pro	Ala	Ala	Ile	Lys	Lys	Thr	Ile	Leu	Asp	Lys	Val	Lys	Leu
		275					280					285			
Asp	Ser	Pro	Ala	Gly	Thr	Ala	Leu	Ser	Pro	Ser	Gly	His	Thr	Lys	Leu
		290				295					300				
Leu	Pro	Arg	Ser	Leu	Ala	Pro	Ala	Gly	Lys	Asp					
305					310					315					